Claims

We claim:

35 1. A method to detect expression of a first transgenic nucleic acid molecule in a sample having either (a) a detectable amount of mRNA transcribed from a second transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said mRNA, said method comprising providing a complementary DNA of the mRNA, amplifying said complementary DNA and hybridizing said complementary DNA with at least one oligonucleotide designed to hybridize to said second transgenic nucleic acid molecule, whereby said hybridizing indicates the expression of said first transgenic nucleic acid molecule in the sample.

36 2. A method according to claim 1 further comprising quantitation of mRNA transcribed from said second transgenic nucleic acid molecule.

37 3. A method according to claim 1 wherein said second transgenic nucleic acid molecule which is selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

38 4. A method according to claim 1 wherein second transgenic nucleic acid molecule is selected from the group consisting of a Petunia HSP70 5' untranslated leader sequence, a wheat fructose 1,6-biphosphatase 5' untranslated leader, a 3'untranslated sequence from the 3' end of the *Pisum sativum* rbcS E9 gene, a 3' untranslated sequence from the wheat ubiquitin gene and a 3' untranslated sequence from the nopaline synthase gene.

39 5. A method according to claim 1 wherein said second transgenic nucleic acid molecule has a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID 35.

40 6. A method according to claim 1 wherein the at least one oligonucleotide is a sequence which is at least substantially identical to a molecule selected from the group consisting of SEQ ID NO: 7 to SEQ ID NO: 12 and SEQ ID NO: 26 to SEQ ID NO: 28.

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41 7. A method according to claim 1 wherein the amplifying is carried out by a method selected from the group consisting of PCR or RT-PCR.

42 8. A method according to claim 2 wherein the quantitation of mRNA is determined by a method selected from the group consisting of quantitative RT-PCR or competitive quantitative RT-PCR.

43 9. A method according to claim 1 wherein said second transgenic nucleic acid molecule comprises at least 100 base pairs of consecutive sequence having substantial identity to a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO 32, SEQ ID NO: 33 and SEQ ID 35.

44 10. A method according to claim 1 wherein said at least one oligonucleotide comprises at least 15 bases substantially identical or complementary to a consecutive sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID 35.

45 11. A method according to claim 1 wherein said at least one oligonucletide has a detectable label.

46 12. A method according to claim 11 wherein said label is selected from the group consisting of a fluorescent label, a digoxigenen-dUTP label, a biotin label, and a radiolabel.

47 13. A method according to claim 1 wherein said at least one oligonucleotide comprises a primer pair and a probe designed to hybridize to a nucleic acid molecule in a 5' nuclease assay.

48 14. A method according to claim 13 wherein each of said primer pair used in said amplification comprises 15 to 30 bases identical or complementary to a consecutive sequence of a second transgenic nucleic acid molecule having a sequence selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences and wherein said probe comprises 15 to 30 bases complementary or identical to a second transgenic nucleic acid molecule having a

sequence selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

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15 A method according to claim 1 further comprising Southern Blotting, Northern Blotting or RNAse protection assay.

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16. An amplification kit for the detection of a transgenic nucleic acid molecule comprising at least one primer pair and a corresponding labeled probe which hybridizes to a nucleic acid molecule selected from the group consisting of a marker selected from the group consisting of a 5' untranslated region selected from the group consisting of Petunia HSP70 5' untranslated leader sequence and wheat fructose 1,6-biphosphatase 5' untranslated leader, a 3'untranslated sequence selected from the group of a 3' end of the *Pisum sativum* rbcS E9 gene, a 3' untranslated sequence from the wheat ubiquitin gene and a 3' untranslated sequence from the nopaline synthase gene.